1 ATGAGCCAGC CCAGGCCCCG CTACGTGGTA GACAGAGCCG CATACTCCCT 51 TACCCTCTTC GACGATGAGT TTGAGAAGAA GGACCGGACA TACCCAGTGG 101 GAGAGAAACT TCGCAATGCC TTCAGATGTT CCTCAGCCAA GATCAAAGCT 151 GTGGTGTTTG GGCTGCTGCC TGTGCTCTCC TGGCTCCCCA AGTACAAGAT 201 TAAAGACTAC ATCATTCCTG ACCTGCTCGG TGGACTCAGC GGGGGATCCA
251 TCCAGGTCCC ACAAGGCATG GCATTTGCTC TGCTGGCCAA CCTTCCTGCA 301 GTCAATGGCC TCTACTCCTC CTTCTTCCCC CTCCTGACCT ACTTCTTCCT 351 GGGGGGTGTT CACCAGATGG TGCCAGGTAC CTTTGCCGTT ATCAGCATCC 401 TGGTGGGTAA CATCTGTCTG CAGCTGGCCC CAGAGTCGAA ATTCCAGGTC 451 TTCAACAATG CCACCAATGA GAGCTATGTG GACACAGCAG CCATGGAGGC 501 TGAGAGGCTG CACGTGTCAG CTACGCTAGC CTGCCTCACC GCCATCATCC 551 AGATGGGTCT GGGCTTCATG CAGTTTGGCT TTGTGGCCAT CTACCTCTCC 601 GAGTCCTTCA TCCGGGGCTT CATGACGGCC GCCGGCCTGC AGATCCTGAT 651 TTCGGTGCTC AAGTACATCT TCGGACTGAC CATCCCCTCC TACACAGGCC 701 CAGGGTCCAT CGTCTTTACC TTCATTGACA TTTGCAAAAA CCTCCCCCAC 751 ACCAACATCG CCTCGCTCAT CTTCGCTCTC ATCAGCGGTG CCTTCCTGGT 801 GCTGGTGAAG GAGCTCAATG CTCGCTACAT GCACAAGATT CGCTTCCCCA 851 TCCCTACAGA GATGATTGTG GTGGTGGTGG CAACAGCTAT CTCCGGGGGC 901 TGTAAGATGC CCAAAAAGTA TCACATGCAG ATCGTGGGAG AAATCCAACG 951 CGGGTTCCCC ACCCCGGTGT CGCCTGTGGT CTCACAGTGG AAGGACATGA 1001 TAGGCACAGC CTTCTCCCTA GCCATCGTGA GCTACGTCAT CAACCTGGCT 1051 ATGGGCCGGA CCCTGGCCAA CAAGCACGGC TACGACGTGG ATTCGAACCA 1101 GGAGATGATC GCTCTCGGCT GCAGCAACTT CTTTGGCTCC TTCTTTAAAA 1151 TTCATGTCAT TTGCTGTGCG CTTTCTGTCA CTCTGGCTGT GGATGGAGCT 1201 GGAGGAAAAT CCCAGGTGGC CAGCCTGTGT GTGTCTCTGG TGGTGATGAT 1251 CACCATGCTG GTCCTGGGGA TCTATCTGTA TCCTCTCCCT AAGTCTGTGC 1301 TAGGAGCCCT GATCGCTGTC AATCTCAAGA ACTCCCTCAA GCAACTCACC 1351 GACCCTACT ACCTGTGGAG GAAGAGCAAG CTGGACTGTT GCATCTGGGT 1401 AGTGAGCTTC CTCTCCTCT TCTTCCTCAG CCTGCCCTAT GGTGTGGCAG 1451 TGGGTGTCGC CTTCTCCGTC CTGGTCGTGG TCTTCCAGAC TCAGTTTCGA 1501 AATGGCTATG CACTGGCCCA GGTCATGGAC ACTGACATTT ATGTGAATCC 1551 CAAGACCTAT AATAGGGCCC AGGATATCCA GGGGATTAAA ATCATCACGT 1601 ACTGCTCCCC TCTCTACTTT GCCAACTCAG AGATCTTCAG GCAAAAGGTC 1651 ATCGCCAAGA CTGTCTCCCT GCAGGAGCTG CAGCAGGACT TTGAGAATGC 1701 GCCCCCACC GACCCCAACA ACAACCAGAC CCCGGCTAAC GGCACCAGCG 1751 TGTCCTATAT CACCTTCAGC CCTGACAGCT CCTCACCTGC CCAGAGTGAG 1801 CCACCAGCCT CCGCTGAGGC CCCCGGCGAG CCCAGTGACA TGCTGGCCAG 1851 CGTCCCACCC TTCGTCACCT TCCACACCCT CATCCTGGAC ATGAGTGGAG 1901 TCAGCTTCGT GGACTTGATG GGCATCAAGG CCCTGGCCAA GCTGAGCTCC 1951 ACCTATGGGA AGATCGGCGT GAAGGTCTTC TTGGTGAACA TCCATGCCCA 2001 GGTGTACAAT GACATTAGCC ATGGAGGCGT CTTTGAGGAT GGGAGTCTAG 2051 AATGCAAGCA CGTCTTTCCC AGCATACATG ACGCAGTCCT CTTTGCCCAG 2101 GCAAATGCTA GAGACGTGAC CCCAGGACAC AACTTCCAAG GGGCTCCAGG 2151 GGATGCTGAG CTCTCCTTGT ACGACTCAGA GGAGGACATT CGCAGCTACT 2201 GGGACTTAGA GCAGGAGATG TTCGGGAGCA TGTTTCACGC AGAGACCCTG 2251 ACCGCCCTGT GA (SEQ ID NO:1)

FEATURES:

JAN 1 5 2003

Start Codon: 1 Stop Codon: 2260



HOMOLOGOUS PROTEINS:

Score	Ε
476	e-133
471	e-131
451	e-125
448	e-124
447	e-124
434	e-120
418	e-115
365	1e-99
362	1e-98
357	4e-97
	476 471 451 448 447 434 418 365 362

BLAST to dbEST:

gi|8630793 /dataset=dbest /taxon=960...

Score

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:
Expression information from BLAST dbEST hits:

gi|8630793 Human head-neck

JAN 1 5 2003 S 1 MS 51 VV 101 VN 151 FN 201 ES 251 TN

Docket No.: CL000861
Serial No.: 09/749,589
Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

```
1 MSQPRPRYVV DRAAYSLTLF DDEFEKKDRT YPVGEKLRNA FRCSSAKIKA 51 VVFGLLPVLS WLPKYKIKDY IIPDLLGGLS GGSIQVPQGM AFALLANLPA 101 VNGLYSSFFP LLTYFFLGGV HQMVPGTFAV ISILVGNICL QLAPESKFQV 151 FNNATNESYV DTAAMEAERL HVSATLACLT AIIQMGLGFM QFGFVAIYLS 201 ESFIRGFMTA AGLQILISVL KYIFGLTIPS YTGPGSIVFT FIDICKNLPH 251 TNIASLIFAL ISGAFLVLVK ELNARYMHKI RFPIPTEMIV VVVATAISGG 301 CKMPKKYHMQ IVGEIQRGFP TPVSPVVSQW KDMIGTAFSL AIVSYVINLA 351 MGRTLANKHG YDVDSNQEMI ALGCSNFFGS FFKIHVICCA LSVTLAVDGA 401 GGKSQVASLC VSLVVMITML VLGIYLYPLP KSVLGALIAV NLKNSLKQLT 451 DPYYLWRKSK LDCCIWVVSF LSSFFLSLPY GVAVGVAFSV LVVVFQTQFR 501 NGYALAQVMD TDIYVNPKTY NRAQDIQGIK IITYCSPLYF ANSEIFRQKV 551 IAKTVSLQEL QQDFENAPPT DPNNNQTPAN GTSVSYITFS PDSSSPAQSE 601 PPASAEAPGE PSDMLASVPP FVTFHTLILD MSGVSFVDLM GIKALAKLSS 651 TYGKIGVKVF LVNIHAQVYN DISHGGVFED GSLECKHVFP SIHDAVLFAQ 701 ANARDVTPGH NFQGAPGDAE LSLYDSEEDI RSYWDLEQEM FGSMFHAETL 751 TAL (SEQ ID NO:2)
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FEATURES:

Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 3 1 153-156 NATN 2 156-159 NESY 3 580-583 NGTS

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site

Number of matches: 2 1 45-47 SAK 2 445-447 SLK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site

Number of matches: 2 1 7-15 RYVVDRAAY 2 447-454 KQLTDPYY



[5] PDOC00008 PS00008 MYRISTYL N-myristoylation site

Number of	matches:	10
1	77-82	GGLSGG
2	78-83	GLSGGS
3	89-94	GMAFAL
4	103-108	GLYSSF
5	335-340	GTAFSL
6	435-440	GALIAV
7	481-486	GVAVGV
8	485-490	GVAFSV
9	581-586	GTSVSY
10	681-686	GSLECK

			<u>ucture</u>	<u>and domains:</u>
Helix	Begin	End	Score	Certainty
1	51	71	0.893	Putative
2	82	102	1.020	Certain
3	107	127	1.729	Certain
4	130	150	1.497	Certain
5	186	206	1.723	Certain
6	228	248	1.517	Certain
7	256	276	1.898	Certain
8	288	308	1.252	Certain
9	338	358	1.568	Certain
10	383	403	1.304	Certain
11	412	432	2.345	Certain
12	469	489	1.997	Certain
13	619	639	1.146	Certain

OIP JAN 1 5 2003 RADEMAR

Docket No.: CL000861 Serial No.: 09/749,589 Inventors: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER...

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BLAST Alignment to Top Hit:
>gb|AAF81911.1|AF279265_1 (AF279265) putative anion transporter 1 [Homo
sapiens]
          Length = 738
Score = 476 bits (1224), Expect = e-133 Identities = 263/724 (36%), Positives = 428/724 (58%), Gaps = 36/724 (4%)
 Frame = +3
Query: 54
            LFDDEFEEKDR--TYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLL 227
            L + EE R + P + R +CS A+ A++ LPVL WLP+Y ++D+++ DLL
            LNQEHLEELGRWGSAPRTHQWRTWLQCSRARAYALLLQHLPVLVWLPRYPVRDWLLGDLL 74
Sbjct: 15
Query: 228
            GGLSGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVG 407
                   +Q+PQG+A+ALLA LP V GLYSSF+P+ YF G
                                                           + GTFAV+S++VG
            SGLSVAIMQLPQGLAYALLAGLPPVFGLYSSFYPVFIYFLFGTSRHISVGTFAVMSVMVG 134
Sbjct: 75
            NICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVA 587
Query: 408
                LAP+
                           A N+S ++ A +A R+ V++TL+L+Q+GLG+FGFV
            SVTESLAPQ-----ALNDSMINETARDAARVQVASTLSVLVGLFQVGLGLIHFGFVV 186
Sbjct: 135
            IYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASL 767
Query: 588
             YLSE +RG+ TAA +Q+ +S LKY+FGL + S++GP S+++T +++C LP + ++
            TYLSEPLVRGYTTAAAVQVFVSQLKYVFGLHLSSHSGPLSLIYTVLEVCWKLPQSKVGTV 246
Sbjct: 187
            IFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQ 947
Query: 768
            + A ++G LV+VK LN + ++ PIP E++ ++ AT IS G + ++ + +VG I
            VTAAVAGVVLVVVKLLNDKLQQQLPMPIPGELLTLIGATGISYGMGLKHRFEVDVVGNIP 306
Sbjct: 247
Query: 948
            RGFPTPVSPVVLQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSN 1127
                PV+P
                       + ++G+AF++A+V + I +++G+ A +HGY VDSNQE++ALG SN
Sbjct: 307 AGLVPPVAPNTQLFSKLVGSAFTIAVVGFAIAISLGKIFALRHGYRVDSNQELVALGLSN 366
Query: 1128 FFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGA 1307
              G F+ + C++S +L + GG SQVA SL +++ ++ LG + LPK+VL A
Sbjct: 367 LIGGIFQCFPVSCSMSRSLVQESTGGNSQVAGAISSLFILLIIVKLGELFHDLPKAVLAA 426
Query: 1308 LIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQ 1487
            +I VNLK L+QL+D LW+ ++ D IW+V+F ++ L+L G+ V V FS+L+VV +
            IIIVNLKGMLRQLSDMRSLWKANRADLLIWLVTFTATILLNLDLGLVVAVIFSLLLVVVR 486
Sbjct: 427
Query: 1488 TQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFANSEIF------ 1637
TQ + L QV DTDIY + Y+ A++++G+K+ + +YFAN+E + Sbjct: 487 TQMPHYSVLGQVPDTDIYRDVAEYSEAKEVRGVKVFRSSATVYFANAEFYSDALKQRCGV 546
Query: 1638 ------RQKVIAK--TVSLQELQQDFE-NAPPTDPNNNQTPAN-GTSVSYI----- 1760
                    ++K++ K + L++LQ++ +
                                                         N TS+ +
Sbjct: 547 DVDFLISQKKKLLKKQEQLKLKQLQKEEKLRKQAASPKGASVSINVNTSLEDMRSNNVED 606
Query: 1761 -----TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGI 1925
                        A + ++AP + S + A P FH+LILD+ +SFVD + +
                   SD
Sbjct: 607 CKMMQVSSGDKMEDATANGQEDSKAP-DGSTLKALGLPQPDFHSLILDLGALSFVDTVCL 665
Query: 1926 KALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQAN 2105
                    + +I V+V++ H+ V + + G F D S+ KH+F S+HDAV FA +
Sbjct: 666 KSLKNIFHDFREIEVEVYMAACHSPVVSQLEAGHFF-DASITKKHLFASVHDAVTFALQH 724
Query: 2106 ARDV 2117
             R V
Sbjct: 725 PRPV 728 (SEQ ID NO :4)
Hmmer search results (Pfam):
Model Description
PF00916 Sulfate transporter family
PF00189 Ribosomal protein S3, C-terminal domain.
```



Docket No.: CL000861 Serial No.: 09/749,589 Inventors: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER...

Parsed for domains:

Model	Domain	seq-f	seq-t	 hmm-f	hmm-t		score	E-value
PF00916	1/1	187	497	 1	328		254.5	1.5e-72
PF00189	1/1	651	661	 79	89	.]	3.3	8

JAN 1 5 2003

R RADEMBER

1 CTGGGTTCCT ATGTGGGGAG GTCATGCTCC CCACTCATTG AGCCCCCCCA 51 GGCAAACCAC CTGGACAGCC AGACCCATGC AGACTCTGGA GCAGGTGGAG 101 AGGAAGAGTG AGACCACCCC GCCTCACGGG CGGTGAAGGG CCGGCAGCCT 151 CTGAATAGTC TCTGCTAGGA GGTAGAAAGC ACCCTCCCAT CTTAATCATA 201 GTAATCATCG CCACTACCAT TTACTGGGTG CCTATAAAAG GCCAGCCTCT 251 TCATACACAT GATCTCACTG AATCCTCATA GCATCTGCCT GCGACTGTTA 301 TTATCCCCAT TTACAGATGA AGAAACTGAA TCTTTGAACC CAGGTCATCT 351 GGCTCTCAAA CTTGTGCTGT TTTCCCTAAG CCACCCGGTC TCTCATTTCT 401 CCCACTGAAA TGTCTCACAT GCCATTGCCC TTACTCATTT CTGCCCATGT 451 CTCCTCCAAA ACACCATTTA TCAATTCGCT CAACAAGTAT GTGTTGAGTA 501 CACACTAAGG GCCAGGCGAG GGGCTGGGCA CAGGCGCTGG GGGTAGGTTC
551 ATTCTCCCAC CTTCGCTTCT GCTGGGTATC ACCTGTGGG TCTTGCCGGG
601 CATCCCACCC TCACCTGTAG TTCAAGTGGA CCTTGGGATC CCAAGACCAA 651 ATGAATGGAA TGCACCAGCC CAGCCTTCAC CAACTTGAGC ACAATCTTAT
701 TCATAATAGA AACTCACATT TGCATCACAC TTTACATTTT ACACAACCCC
751 TTCTTATCCA TTAACTCATT TGATCTTCAC AACAACCCTG TGAGATATGT 801 CTGTTACTCC CACTTTAGTG ATACAGAATC TGAGGTTTGA AAAGTAATGC 851 TGACCATTCT GCCTCATTAA TAAAAGCAGG ATTAACCCAG GCTCCTGGAC 901 CCTTCCACAA AAGGCATTAA GCAACCTGCT CCCCTCTGAC AACCTCCCCT 951 GTCACCCAGG CTCTCCTCTG GGAAGTTGGG GGCATCTCTA GCCCCCAAGT 1001 AGTTACTCAT TITCAACCCC ATCTCAAATC TTTTGCCAAA CTGGCCACAG 1051 CCACCCCACA CTCCCCACCT CCCAGATACA AATCCTCACT CTAAGCCTTC 1101 CCCATCTCTT TCTTCTCTGT CCTTCTTTCT CTGTGGTCCT CTGAGCAACT 1151 TCTCCCAGCT CTGGGAGGTA GAGGGGAGGT GGGAGACCCA GTAATTGGAA 1201 GAGGGAGGGG GAAAGGTTCC TACAGGGAAC TCCTCCGGGC CTCAGGGGCC 1251 CTGGCACTCA GCTCTGCCCA TCTCAGCTCC TGGAACGTCA GCCAGGTTGC 1301 GCAAAAAGTG AGGAGGAGAG GAGCGGCAGT ACACAAGGGT GGGGGAAAGA 1351 TTAGGCACAG GAAGCCGTGG GAGAGAGAGC CGGCAGGTGG ACCATCCTGG 1401 TTTCCCCACA CACACCATTG TCCCCCTGGG AAACCTGTTG GTGAAGTTCT 1451 AGATGTCTTA TCCAAGAAGG GTCCTCTTGA GGTCATCTCA GCTATCCCCC 1501 TGCCTCTAGG CAAGCTGTTT TCTGTTTCTT CCAAGCTGAC TGGCTGAATG 1551 GTAGGAGCCT TTCTGCCAGG GAAACTAAGG TCTGGGAAGG GAGTATGGCT 1601 TGTGGGGACA CCAGGGGTCA GGGGAGGGGA GGGTCCACCT GCTGAATCAA 1651 GTGGGGCCTC CTGCCCTCGT GATTCCCCTT TGCCTGGTGC TCAGTGGGGG 1701 TGATGGTGAC GCCACAGGTG TGGAGTGCCA GCCACGTGCT GAGCGCCAAG 1751 CAAAACAGCC AGGGTGAGTC TATGCATCAT CAGTGCCTGG GAAGGAAGGC 1801 CACTGCGAGC AGGGAGTCTG ACGGAAAAAC TTGACAGAGG GAAGGGAGGC 1851 ACCTTGCTTT ATCGGGCGG GGAAGGCCAG AATAAAACTC TGCTACTGCA
1901 AGGACCAGAG AGAGAAGGCC TGGGCTGGCA CTAGGGAGGG ATGTTCCCTC
1951 ACCCTCCCCT CCTCTGCTTC TCCCAAAGCT TGTAAATGCC CCAGATATGA 2001 GCCAGCCCAG GCCCCGCTAC GTGGTAGACA GAGCCGCATA CTCCCTTACC 2051 CTCTTCGACG ATGAGTTTGA GAAGAAGGAC CGGACATACC CAGTGGGAGA 2101 GAAACTTCGC AATGCCTTCA GGTAACTGGT CCAGAGCCCA GACTTCTGCC 2151 TCCTCTGCTC CCTACCAAAA TCCTTTCTGC ACCAGGACAC GGCTTCTGCA 2201 CTGGTATCCC TAAGATGGGG TTAAGGGAAG CCCTGGGGAA GTGAGGTTCT 2251 GAATGATGAA TTTAAGATCC TACAACCTCA TCTGTACTGA GACCCCCAGG 2301 GAGGATGGGG AGCAGGAGCA AGAACCATCC AGAAGGGTTA TATGGCATTC
2351 CCAAACCCCT GCATGGCATC TCCCATATTC TCAATTCACC CGGGTCTCTC
2401 TGGGTTTGTT AAGGCATGGT AGATGAGCAT CTACGTTATG GAGGGGTGGG
2451 GAGCATCAGA GCCCTTACTC CATGCCCTGT TCCCTCCTTA CAAAAAATAC 2501 CTGAAGTTAC CATCACCCCA GGTTCTTTGT CCTTTCCCTC CCGGATGTTC 2551 CTTCCTCCAC TTGGTCCAGA GAATGCCAAA AGGAGGCCCT AAATTTCTGA 2601 ACTITCCTGA GGGGACCTAC CAGGGTGTAG TCCTACCAGC GCCCAGGGTC 2651 TTTCCACTCT CATCTCCCTG GAAATGCGAT GGTGGGTATG AAACCTTGTC 2701 CCTAAGTAGG CGCTACACAA GGTGATCCAT ACCCACACCC CAGGAGGCTG 2751 GGGCTGCGGG TGTCACCCTC CCCATTCCCA GACTCCTGGC AGACCTCCTC 2801 TGGCCCAGCT ATAGGCCAAC TCACTCTCCC TCACTCCCTT GGGGAAACGG 2851 CTGATTCAGT TACCTGGATT GAGGTCACTG GCAATGGCTG AAGTGGAGAC 2901 GCAGGTGGAA CTGGTTCAGG CCGGGGGAAT CACCCACTTG AGTTTGTACT 2951 AAAAGCCCCA GCCCAGCCCT GTTTCTCTTG GGAGGCTCCA TTTCTGCCCA 3001 GTTACAGTCT GTCCTCACAG CTGTGCTCCT CAGACAGGTG GTCTCTGCCA 3051 GTCTTTGTGC CCAAGACTTT AGGGCACAAA GTCTGAGGAT GAGAAGATCT 3101 GCTATTGTCC TAAAAGATTA GGATAATGAA AGCTGTAAAG GGATATAGCA 3151 AACTAACAAT TCCTATGATA CTGGCATGAG AGCCTTGAAC AGTGCCTGGC 3201 ATAGAGAAGG TGCACCAATA AATATTTGTT TCATGAATGA ATGAATGAAT 3251 GAATGTCTAG AAAGCTAATC CCTCTCAGCC TCTGTTTCCA GTTCTTCTTT 3301 CAAGCTTCAG ATTGCTTTGC CCAACATACA GCAGACTTGC AAGTAAGGTT 3351 GGGCATGGAC TAGCCCTCAA ATGAGTTGTT TTTCTTTCCC TAGCCAGCTC

JAN. BADEMARKS 3401 TCTATTCATA AGTCCGGCTT TCTCTGCCAC AAACAGACCT GATGGAGCCC 3451 CTGCAGGGCT GGTTCTCTCT TCAAGCAAGG CTTTAGAGTT GCATTAAGCA 3501 ATTTATCCCC CGTCCACCTC CCCTTCCAGC ATCCCAGGGA TGGCAGAGGC 3551 ACCCATGAGC CCCAGAAGGG ACAGGGGGTA AGATATTGAT GATGATGCTT 3601 TTTCTTGGAG TGTTAGTTGG AAGAGAAAAT CTGCCCAGAC TTTCCAAGGT 3651 ACAAAGCATT GTCTTTGTTG GTTTCAGTCT TGGGTGACAT CCAGGGGACC 3701 GAGTGTCAGG GAAACTATTG TTGAGCAAGA GCAAAGAGCA GGAATTGGTG 3751 CTGGGCAGGA AAGGAAGCCT CATCAGAGCA GGCCAGTGAG TCACCAAATG 3801 GGCCCTAAGT ATTTGAGTTC CCTCAACTGG GAGAAGGAAA GCAAATGCCC 3851 CTCACCCACT TCCAGTCATC AATCCACCGG CTGTCACCCT TGAGTTTGTA 3901 AGCCCTTGTT CCTACCGCTC CTGAGTTTCT ATGAAAGGAC CTTGAGGTGT 3951 TCAACAAACA GGGAAGGGAT CAACTCTCCC CACCCTGCGT TGACCAATGA 4001 ATTCTTCCCT CCTCTGCTGC CCAGTGAATT AACAGGAGAA AGAACTCCGG 4051 TATTGGAGTT ACCACACATA AAGGATAGTG AGTCAGCAGA GTGCACCCTG 4101 CAGGAACAAT AGAGCCTTCC TTTTCAAGGA AGTTCTAAGA AAAATGGCAG
4151 CAGGCAGGCC CCACTCGGGT GTATTCACTC ATTCATTAT TCAACAAATA 4201 TTTACTAAGT GCCCCTGTGC AAGGCTCGAG GTGTACAAAG ATGAACAGGA 4251 GAGCTAGACT TCTTGCCATG CGTGGTGGGG TTTGCTGCCT AGTGGGAGAG 4301 ACAGACAAAA AGCAAGGAAT GCACACAG GATGCACACA CAGCGGCAGG 4351 AACCAAGGTG CAGTTACCCA GGCCTGGGAT CAGACAGACA GGACTCAGAG 4401 GAGACTTTCC CAGAGAAAAG CCATCTGAGC CAAGGGATGG ATCTGATACC 4451 TCCGAAGGCT GAGCCACCAT AACACTCATA CCTTTAAGCC AAGTCTTATA
4501 AACTCCCCAG GTAAGCAGCT GGCAGTCAGA AGACCTCCAG CTAATGCCCA 4551 GGACAAGTTG ATGAGCTCTC AAGAAAAAGT TCCTGCCTTT TCTTCTCAAT 4601 ATCCCTGGCA CACAGTTCAG TGAATTTTGA ATGAACCAAT GAATGAAATG 4651 AGCAGGATAT GATAATCCCT CTCCAACACG GAATGTCCAA GCCATGCAGA 4701 GCCGACTGGA AATTITCCCC GTTCCCTTCC AGATGTTCCT CAGCCAAGAT 4751 CAAAGCTGTG GTGTTTGGGC TGCTGCCTGT GCTCTCCTGG CTCCCCAAGT 4801 ACAAGATTAA AGACTACATC ATTCCTGACC TGCTCGGTGG ACTCAGCGGG 4851 GGATCCATCC AGGTCCCACA AGGTGAAGGG GCTCCTTCAG CCAGGCCTGG 4901 ATTGCCACTC CCCTCACCAT TCCTCTCCTC ATCCCCACTC CATCCCTCTG 4951 TGATCCCCAT AAGCTAGTCA TGCTGCTGAG CTTCAGTCTC GTTGTCCTCT 5001 GCAGGCATGG CATTTGCTCT GCTGGCCAAC CTTCCTGCAG TCAATGGCCT 5051 CTACTCCTCC TTCTTCCCCC TCCTGACCTA CTTCTTCCTG GGGGGTGTTC 5101 ACCAGATGGT GCCAGGTAAG GCCTCTCCCC TCTGGGCAGG CAGGATGACC 5151 CAGACCACAA GGATGGGAGG TGTGGCAAAG GGGCCTCGGG AGATTTTCCA 5201 TCTGCATTCT CCTGGAGTTG TTCCTGGTCA GTCCTAGGGG AATGGTCACT 5251 GTGAATGTCA TTTCCAGGTC CTCGGTGACC TTGGAGAAAC CACTGAGCCT 5301 CTTTGAGTTC AGTTAGCATT ACCTGTTCCA TCTTCCTCCT AGGAATGAGA 5351 GGAAGACTTA GCAGAACAAG ATATACCATA TGCTATAACA TGCTTAAACA 5401 GATGTGAGAA ATCACCATCT AACTCCCTGG TTGGTCCCAG CCGGCCACTA 5451 CAGGGACATT TGGACTTCTC TGGTGCTAAG TGAGATGGAG GAAAGCCTGG 5501 TCACAAGGGC TGGTTTCTGG TTCAGGCTCT GCTTATATTT CTTATTTCTG 5551 AGTTCATTTT CTCACGTGTC CTGTATGACA ATATTGACCA TTGGGGTAAA 5601 AGCACCTTGA AAAGCATAGA TCATGGTTAG AGTGAGTGGT TGTTATTATT 5651 GTGTTGGAGA AGAGCCTTGG AGGTGCAGGG ATCCATCCCC CTGGGGTCGG 5701 GAAGCATTCC TGGGCCCCTT TCTGGTTTCC ATCGGTGTGG TTCAAACCTC 5751 TGATTTTTGC TGGCTGGGTG GGGCACCACA GGTACCTTTG CCGTTATCAG 5801 CATCCTGGTG GGTAACATCT GTCTGCAGCT GGCCCCAGAG TCGAAATTCC 5851 AGGTCTTCAA CAATGCCACC AATGAGAGCT ATGTGGACAC AGCAGCCATG 5901 GAGGCTGAGA GGCTGCACGT GTCAGCTACG CTAGCCTGCC TCACTGCCAT 5951 CATCCAGGTG AGGGGGCAGC CCCCAACCCT GCTAGAAGGG CATCAGACCA 6001 CCCTGCCCCT CCCTCAAAGC CTTAGCTTTG ATGCTAAATC TGATTTAGGG 6051 GGCTGGGTGT GGAGGCTCAT GCCTGTAATC CCAGCACTTT GGGAGGCTGA 6101 GGAGGGTGGA TCACTTGAGG TCAGGAGTTT GAGACCACCT TGACCAACGT 6151 GATGAAACCC CATCTCTACC AAAAATACAA AAATAATCCA GGCTTGGTAG 6201 TATGCGCCTG TAGTCCCACC TACTCAGGAG GCTGAGGCAG GAGAATCACT 6251 TGAATCCGGG AGGCAGAGGT TGCAGTGAGC TGAGATCGCG CCACTGCACT 6301 CCAGCCTGGG TGACAGAGCG AGACTCCGTC TCAAAAAAAA AAAAAAAAA 6351 AAAAAAAAA CCCAAGTTAG GGCTCACCTC CTCCCTCCTC CCCATCCCAG 6401 GGCTAAAGTG AACCTTGAAA ATTAACAGTA TCTCCTCATC TGCATGTAGC 6451 AGGACCATAC AAAAAAACAA CAGCTGTACC TGGTTAAACT GTCCTGAGCT 6501 TTAAACCTGT AAAAGACTCA CAGCCTCTCT CCATTATCCC GTGGAGAAAC 6551 CCAACTCTCT GCCAGCATAG TCTTGCAGAC TGCTAATTTT CTCTAACATC 6601 CCTCACTCCG CTCCAGCCTC CTCTGCTCCA AGCCACAGCA GCAGTTGCAC 6651 AACATAAATT GAGCTTCTGC AAATGGTTGC AAAGGATTCT GCTAGGTTTT 6701 ATGAAGGGAA GCACAACATG ACAGAATGCA AGAGCAAAAC ACAGTCCCAG 6751 AGAGCGCCTT TTCATTCACT CATTCATTCG GTTTTGTGCC AAGAACTAGG

JAN 1 5 2003 R

Docket No.: CL000861
Serial No.: 09/749,589
Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

6801 CTAAACCCTG GGATACAAAG ATAAGTAAGA AAGAGGTCCA ATTCACAAGT 6851 TGCTCACAGC CCAGCAGAGG AAGGAGCCAT GTCAACAGAT AAATTTGTAT 6901 GCAGTGAGAT AAGCAGCAAA GTAGAGCCAT GTACAAAGAC TGTAGGGACA 6951 CAGAGCAGAG TCACGGAGGA CCTCAAAGAG GAGGTGACAC TCCACCTCTC 7001 TTAAAGGATG AGAACTTAAC CAGGAACAAG GTATACAGAG GATGGTCCAG 7051 GCAGAAGGGA ACAGTGCCTA AAAACACTGA GGCCTGAGAG AGTGTGATCT 7101 GCGCAGGCAA AGTAAGGGGC TTGGTGTGGC TGGAGGGTAG AGGGCCCAGA 7151 AGAGGATGGA AAAGTAGGCA GGAGCCAGAC AATGAGATCT GGGGTCTGTT 7201 CTCTGACAGC GACTTTGGGT CTGATTGGCA GTTTATAAGG ATCGTTTGGG 7251 CTACACAATG ATGAGTGGGA GGTGGATTAG AATCAAGGCA GGGGACCTGT 7301 TGGGAGACTC TGCAGAGGCC CAGGCAGGAA TAATGCAGGC GAAGACCAGG 7351 TAGAGAAAGA GATGGGGCTG GACTTGAAAA GAATGTTTTA CCAGGAGCTT 7401 GGTGATAGAC TGGATGTGGG AGGTAAGGGA GGATGACTCT CAAGTTTTTG 7451 GTTGGGCAAC CAGGTTAATG ATGGTGTCAT TTACTGAGAG AGAAAACACT 7501 GGGGGAGGAC TAGACTTATT TTACAGATAA GCCAAAGCCA GAGAGGTGAT 7551 GTGACAGAAA GGCCCATGCT CTAAAGGAGC TGAAGGTCTG ATGGCAGCCA 7601 TGTAGAGCAC AGTGAAGGGC AGGTGAAGGT CACAGATGGT CCAATTCCCT 7651 CAAGCTACTG CTACGCTAGG ACTGCACGGA GCTCCAGACC TGCGTGTGTG 7701 TGGGGCGGGT CGTTGGAACT GCTGAACCAC ATTGGTCTTC CGCCACCAAC 7751 CACCCTTTTC CTCCTCTCAG ATGGGTCTGG GCTTCATGCA GTTTGGCTTT 7801 GTGGCCATCT ACCTCTCCGA GTCCTTCATC CGGGGCTTCA TGACGGCCGC 7851 CGGCCTGCAG ATCCTGATTT CGGTGCTCAA GTACATCTTC GGACTGACCA 7901 TCCCCTCCTA CACAGGCCCA GGGTCCATCG TCTTTGTGAG TCTGGGGATG 7951 CACCCCTGCC ATTGGAGCAA GGCTCCAGCA GACACATGAG GAGGATGTAC 8001 TGTTTTAAGA TGTCGTGAGC TCCTCATTGC AAGGGCTGGC TTAGCTGTTG 8051 TTCAGAGAGG ATTCTGAGGG GGTTTCTGTC TTGGGAGGGT CAAAGTCATG 8101 ACTCACAGAG GTTCTTGGTA GTTAATACCT GCAGAAAAGA GCTGTACATT 8151 CTCCGCCAGT TCCCCATTCT AGTGCCTCAA CCCCTCCCTG CCTGGAAAGT 8201 CCTGCCTTAT GTCTAATCTC CATCCCTCCT CCTTCAGCCC AAACTCTTCT 8251 AAAGAAAAAG AAAGCATTCC TTTTCTAGCA CAAGTTCCCC ATGTGCCTTT 8301 TGGGAAAGGG CGGTGGGCGA CGGGACAGGG TTCCTGATCA GGGTTTTAAT 8351 TCTGTCTTGG TGTGCCTCCA TTAGCTTTGA TGGCATCCCT TCCCTGGGTC 8401 AGACACCCAA AGGTGGGGTA TTATGGGAAG AAGGGGTGGG AGCCTGTGAG 8451 CATGATGCTC TTTCCCCCAG ACCTTCATTG ACATTTGCAA AAACCTCCCC 8501 CACACCAACA TCGCCTCGCT CATCTTCGCT CTCATCAGCG GTGCCTTCCT 8551 GGTGCTGGTG AAGGAGCTCA ATGCTCGCTA CATGCACAAG ATTCGCTTCC 8601 CCATCCCTAC AGAGATGATT GTGGTAAGGA CCTTGTTCAG AGCTGGGATG 8651 TTGGGGGGCC AGGCTGTGAG ACGAGGAAGC CCCTACCTTT CCTCACCCCA 8701 TCCCCTCAAC TGGCAGCCAG TGGGACAGGA AGTCAGTTGT GAATCCATCC 8751 CATCCCCCGT ATGTGGCGTT TCCTCTCTTT CTACTGCTCT AATAATTCCC 8801 CCTAAGGAGG CAGGGGAGTG GGATTCAGGG TCCCCAGAGA AAAGGGAGAC 8851 TTGAGAGAGA CGCCTGCCCT GGCCCCACCT TAGGGCCAAT CCCCATTCTC 8901 CACTCTGGGG TTTGCAGGTG GTGGTGGCAA CAGCTATCTC CGGGGGCTGT 8951 AAGATGCCCA AAAAGTATCA CATGCAGATC GTGGGAGAAA TCCAACGCGG 9001 GTGAGTCCAG GTGGCCCAGA AGCCTGGCCC ACCCGCACCT CATGCCCCAC 9051 TAAGGCCTGA GCTCGGAGAG GGAGACAAGA TGAACTCTAT GAAAGTGCAG 9101 TCGAAACTGT ATGACACTGA CCATGTATGA ATTATTACTA TTACCGTTTC 9151 CTGAGAAGGG CCGCACAACC AGCCAATGTA GGCTATTTTA TGAGAAATGA 9201 GTCTTAACTG CCACACTCCC CTTATAAATC TCATTCAACT GATGCTGTTA 9251 AACAAAGCCT CTCTGAACAG CCGCTTGCTG GCTCTTTGCC TTGCTCTAAT 9301 GCATTGGTTC TTTGTCCATG TAGAAAGGGA ACTATTAGGT TCAACCAGAT 9351 TCATGAAGCA TCCACTCTGT GCCAGGCACC ATGCTGGGCC CTGGGAGGAG 9401 AGGGGTGACG CTTGTCCTGC AGGGTTGGAA CAGGCAAGGG AGGGAAGACC 9451 ACATAGCACC AAAGGTCTAG GGGTCTGTGG ACTCGTGAGC ATACAGGGTT 9501 CAGAATCTGG GAGTTAACAA ACGAGGCCCT ACCACATACT GGCCCGGGGA 9551 CCTTGGGCAA GTTAGGTTCT CTCAGCCTCA GTTTCCTCCT TTGTAAAACA 9601 GGAGTGATGG TCCCTACCCT ATGGGGTGGT GCTGAGGATT CAGACTGGAT 9651 GGGATAACTT AGGCAAAGAT CCCGGCACAC CATGGGGGCC TGGCTGGTCC
9701 CTGTGGGCTG GTGAAGGACT TGGCTGCCCT CCCCACTCAC ACCCTTGGGT
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Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

10201 AATCCTGTCC CCTCCCTGCA GGAGATGATC GCTCTCGGCT GCAGCAACTT 10251 CTTTGGCTCC TTCTTTAAAA TTCATGTCAT TTGCTGTGCG CTTTCTGTCA 10301 CTCTGGCTGT GGATGGAGCT GGAGGAAAAT CCCAGGTGAG CCTTGTTCTA 10351 GGGGAGTTGG GGGGAGGTGG TAAGAGAACA GTTGCCCCAA AAAAGCCTGG
10401 GCACTGCAAG CCAGGCCAGC TCTTCTCCGA CCCCTTCTTC CCGTACTTAG
10451 TCTCCACTCC ACCAAAGCCA TGGATTGGAA ATAAATCAAG AGCAAAAATT 10501 TCACACCTTC CCTCTATCCC CAACTCTTTC TCGGAATAGG TGGCCAGCCT 10501 TCACACCTTC CCTCTATCCC CAACTCTTTC TCGGAATAGG TGGCCAGCCT
10551 GTGTGTGTCT CTGGTGGTGA TGATCACCAT GCTGGTCCTG GGGATCTATC
10601 TGTATCCTCT CCCTAAGGAA AGAGCCCAGC CATCGAGCAG AAGTCAACGA
10651 AAGACTCCAA TAAGAACAAT CCCTGAGAGT TGTGTGGCAC TTTACGGACC
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10751 GACAATGCAG GTTTTATCCT CCCCATTTTA CAGGTGAAGG AAACTGAGTC
10801 TGAGAGTCTA ACTGCAGCCTT CTGGCCAGA AGTCTAATCC CTAGGCAACA 10851 TGGTCCCAAA CTCCAGCCTT CTGGCCTCAG AGTCTAATCC CTAGGCAACA 10901 TTTGCACCTA CCCACGAGTA CCAGGCTCTT ATATAGCCCA GCTAGGAGGG 10951 CTCTAGGCAT GCGTCATTTA GAGATGAGGG AAGAGAGATA GGGAAAGGAT 11001 GGGGCCAGGA AGGACCCCAT GGCTCTAACG CCAGCACTTT CCAAACCTAA 11001 GGGCCAGGA AGGACCCAT GGCTCTAACG CCAGCACTTT CCAAACCTAA
11051 GGTCGAATGC AGAGATTTGG GGGATCAGC AGGGGAGGTG TTCCAGAACT
11101 CCGTCTCTGT CCTGCCAGGC CTTGGGGTCG GGTATGCGCA GGAGGGCAAA
11151 AAGAAGGGGA GACCCTGGGG TCCTGGAGCA ATGTTCTGCT TCTCTAGTCT
11201 GTGCTAGGAG CCCTGATCGC TGTCAATCTC AAGAACTCCC TCAAGCAACT
11251 CACCGACCCC TACTACCTGT GGAGGAAGAG CAAGCTGGAC TGTGTAAGTA
11301 TCGGGCAGCC TCTGGGTACT GGCCATGCCC CTGCCCTCTC CTCCAACCCC
11351 ACAGCCCTGT CAGCCCTGTC CTAACAATGA ACCCTCTAGT CTGCTGCTTC 11351 ACAGCCIGI CAGCCCIGIC CIAACAAIGA ACCCTCIAGI CIGCTGCTTC
11401 CTAATTAGCA TGAGATGAGT GGTTAAAAGT CCGAGTTTCG AAGTGAAACA
11451 TCCTATGTTC AAACCCTAAC TCAGCCATCT GCTGGCTCCA TGGCCAATAG
11501 CAAGCCCCTT AACCTTTCCC AGTCTTGGTG TCTTAACTGG GCAAATGGTT
11551 ATTITATGCT CTCTGCCTCC CAGGGTTTTC TATGAAGAAG AAGCAAGGTA
11601 ATACAAGTAA ACATGTTGTC TACATCGTAT TTTATACTCA ATAAAGCTTA
11651 GCTATGACTA CTTTATGACA TACAGCATAAA GCCAACAAAA GGAAATGTT 11701 TGTATTTTAA AAAAAAACCT AGAACATAAA GCCAGAGGAC CAAAATCTTG
11751 AGCAAGTTAC TAGACTTCCC TGGGGTTCTA TTTCCTCATC TGTAAATGGG
11801 GGTGAGACTC ATGCAGTCAT GGTTGCGTCA AACGCTGGTT CCGAGGATTA 11851 AATGAGATCC CAGTGGGAAA ACACCGCATG AGCGCAAACA TTCTGCAAAC 11901 ATGACTTATT GTCCTGATTA GTCACACACT CCACCGCATC ATCCGCTGGG 11951 CATAGTAATG AAGGCCAGTG TGTTTTGACG ACACTGCCTT CTCTCCATTT 12001 AAGCCCCACC ATAACCTATG GGAGAGGATT TACTAAACTT TCTTAACGGT 12051 GATGAAACCA AGGCTCAGAA TGGTTAAGTA AATTGTCAAA GGCCACAGAG 12101 GTAGGGAGTG GTAGAGTCTG GATTAAAACT CCAAGTCCTG GACTCCAGAC 12151 CTCTAGGCTG TACTGTCTCA TAGGGAAGGC AGTCTCACCC ACCTAGGGCA 12201 GAGAAGAAAA TCCTTAAAGC CAGAGAAGTG AGTGGCTCAT CTGTGGTCAC 12251 CCAGAGAGAC AGTGATGAGG ACAGGGAGAA AAATTATACC TCAGTTCCCA 12301 GCCCAAGGAT CTGCTTTGAC CATAACCCAA CAAGCCCCCG CTATGGTGGT 12351 ATTTCCTTAG GTTCATATGG CGGCTTTTGT TTCCATTTGA TCTTCACAGC 12401 AATTCTCTAC AGGAATCTGG GCAGATTTAT TTCCTTTAGA GGAATTTCCA 12451 GGTCTTAAAA TCTATAGGGG GCAACTATCA AAACTTCACC CAATGTTGCC 12501 CCCTACCCAC ACACAAAACC AGGCCCCCAG CCGATCAGAA AGCACTGCTG 12551 AGCTCCTGTC AGGGCCCACG CAGCTCGCTG TGAGACAGAG AGAGGGAACT 12601 CACATTTATT GATCACCTAC TGAGCATCCA TCACTAGGCT AGGACCGTCA 12651 CATTCCTTAA CTTTTGAATC CTTTCATGAG GTAGGCATTA TTATTCTCCT 12701 TTTGTTTCAC ATAGCCATTA AAGAACAAAA TTTGGGGCTG GGTGTGCTGA 12751 CTCACACCTG TGATCTAGCA CTTTAGGGGG CTGAGGCAGG AGGATCGCTT
12801 GAAGTCAGGA TTTCAAGGTC AGCTTGGGCA GCTTAGCGAG AGCCGTCTCT
12851 AGAAAAATAAT AAAAGTTAGC TGGGTGTGGT GGCACGTGCC TATAGTCCTA
12901 ACTGCACTGA AAGGTTAGGC GGAGCACAA CTTGGGTTAGC AGAGTTAGGA 12951 GCTCCAGTGA GCTGATCTTG CCACTGCACT ACAGCCTGAG CAACAGAGCA 13001 AGACCCTGTG ACTCCAAAAA CAAACAAACA AACACATTTT GAACCCAAAC 13051 AGATCTGACC CAAGATGCAT GCTCTTATAG ATGCCACCTC CCTGTGTGCT 13101 GGGGCTTCTA CTAAAAACAC AGACAAGATC AGGCAACCAC AGTCAATCTA 13151 AGGGAAAGAG GAAAGTGTAA CCAAAGCACA AATACATAAA ATATTGCAAA 13201 AATGCTATTT AAAGAAAAAA AAGAGAAGAG AGGCTCTGAG GTTGTACTAA 13251 CAGAGAATGG CCTTGGCTAA TCCAGGAAGA CTTCCTGAAA GAGGTTGTTT
13301 TTTCCCCAGG TCTGCTTTTG ACATCTCTCT TTTCACAGTG CATCTGGGTA
13351 GTGAGCTTCC TCTCCTCCTT CTTCCTCAGC CTGCCCTATG GTGTGGCAGT
13401 GGGTGTCGCC TTCTCCGTCC TGGTCGTGGT CTTCCAGACT CAGTTGTAAG 13451 TGATAGCTTC CGCCCTCCTA GGCCCACAGT CGGTTCCCTG GGCCAGCCCG
13501 CAAAGGGCTT CCATGCCACG GCCTGGCTTA GTCCACTGTA CCTTCCACCT 13551 CTGGGCCTGG CACTGGAGGT GCTGCCAGGC CCAAAGAGAG CCCAACCCAG

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Inventors: Karl GUEGLER et al.
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13601 CCAGGACTGT GGGCACAGTC TGGGCTGTTT GACTTCCCAT ATCTTGAAAA 13651 CCCCAGAGAA AGCCAGCATA CTCTTGCTGG GGATGGCTGG GGAGAGGGCA 13701 GTGGCAGAGA AAGGAGGGCA AGGGCAGGTG GTGAGATTCA ACATCCTTCC 13751 AAAGACATTG CCAGAACCCC AAACCAAATG GGACCCCACC CCAGGAGAGC 13801 GCCAGGGTGG AAGACAGAAG CTGTGTTCTA CACACTGGGA GTATTACAGA
13851 GAAGGGGTCT TGGCCAAGGC AGGGAGTACG CTGAATGTTG GGGGAATCCT
13901 ATCTTCTCTT ¢TTGAGAACT CAGAACAAGG AAATGATGAC TTCAGGGCGA
13951 CTCCCACCAC TTCTCCCACC ACTTCTCTCC CCTGCCCTGT GGTCTGGGAG 14001 CTATGTCAAG GACCTGCCTG TCATCCTCAT AGTTATAGGA GGCCACAGGC
14051 CACCAGACAT GTGTCTCCAG TGCAAAAAGA CAGACACAGC AAGTCTGGGG
14101 GTGAGGACAG GACCCCATCC TACCTTGGCT CTGCCCCCGC CCCAGCAGGG
14151 GCACCCTTCC AGGCCCATGT GCCATTAGCA TTCTCTTATG TTTTTCTCTT
14201 CCTGCTTCAT CCAGTCGAAA TGGCTATGCA CTGGCCCAGG TCATGGACAC 14251 TGACATTTAT GTGAATCCCA AGACCTATAA TAGGGTAGGT AATTCAAGCT 14301 TATGACCTCC TTCTTTTGCT CTGCACCACC CCAAGAAGAG GTTGCTTTTT
14351 AAAGCCAATA AAGACATTC TGCAACTTGA GCTCAGTCTC CCTGTCACAG
14401 GCCCAGGATA TCCAGGGGGAT TAAAATCATC ACGTACTGCT CCCCTCTCTA 14451 CTTTGCCAAC TCAGAGATCT TCAGGCAAAA GGTCATCGCC AAGGTAAGGC 14501 TCAGTCCCTG GCGACCAGAG GCTCTGGACA GAGAGTGGCC GGAAAATGGA 14551 AGCAGAAGGG CGGTGGGAGC TGAGAATAGG CCACTCCCAT AGAGGGTGGA 14601 GGTCAAGATT GCTGTTGGCT CTCTCCCTGC AGACAGGCAT GGACCCCCAG 14651 AAAGTATTAC TAGCCAAGCA AAAATACCTC AAGAAGCAGG AGAAGCGGAG 14701 AATGAGGCCC ACACAACAGA GGAGGTCTCT ATTCATGAAA ACCAAGGTGA 14751 ATGAAGGCCA GAAGCAGCCC CGTGCCCTGC, TCTCCTGCCC ATTCTGATAC 14801 TGCCCCCTGT TACTCATGGT ACCCTGGGGG CCCCGCTTCC CACCCTGACA
14851 GGCAAAGACA GAAAGTCTCT GGGAACACTG CCTGGTGGCC GCTGGGCATT
14901 TTTCTTCTTT TTTTTCTTTT TCTTTTTAGA GATGGAATTT TGCTCTTGTC 14951 ACCCAGGCTT GAGTGCAATG GCGTTATCTT GGCTCACTGC AACCTCCACC 15001 TCTGGGGTTC AAGCGATTCT CCTGCCTTAG CCTCCCAAGT CGCTGAGATT 15051 ACAGGTGCCA CCACACCCAG CTAATTTTTG TATTTTTAGT AGATATTGGG 15101 TTTCACCATG TTGGCCAGGC TGGTGTCAAA CTCCTGACCT CAGGTGATCC 15151 ACCTACCTTA GCCTTCCAAA GTGCTGGGAT TACAAGCCTG AGCCACTGCG 15201 CCCAGCCTGG GCATTTTTCT TCTTGGATGA GGTGCTACCA TCTCCCAGGG 15251 AAGCCACTGA ACCCCCAAGG CCCTTCTCCA TTTTCTGGCT AAGATAGGAC 15301 ATGGCCCATG GACTTTTGAA CAACCCAGAG GGGGAACAGC AGTGAATTTC
15351 CTGGGGAACC CAGGCAGCCC AGGGCTAGCA AGGCTGGGGT GGCCATGGCA
15401 GTAATCCTTG TAATCCCAGC ACTTTAGGAG GCCGAGATGG GAGAATCACT 15451 CTCATGAGTT CAGGAGTTCG AGACCAGCCT GCCCAACGTG GCGAAACGCT 15501 GTCTCTACTA AAAATACACA AAAATTAGCC AGGCGTGGTG GTGGGCACCT 15551 GTAATCCCAG CTACTCAGGA GGCTGAGGCA CGAGAATCAC TTGAACCCGG 15601 GAGGCAGAGG TTGCAGTGAG CCGAGATAGT GCCACTGCAC TCCAGCCTAG 15651 GCAACAGAGG GAGACTCTGT CTCAAGAAAT AAAGGAGCTC AGTGTCCCCG
15701 GAGGGGCTTT CTCCCAGAGA GAGTGGGCTT GAGGACTCAG TGCCTCTCTT
15751 GGCTGGGTTCC TCTGGCTTGT TCTGGGTTGT AGGAGACCAA GTTTGCAGGC 15801 CCTGCCTAAG AAAGGGCTTT GGGAGAGGCC TCTCTGGTGG AGCTTTCAGG
15851 GTCTGTGTTC ACCATCACCG AGGCGAGTTA TTCCCCTACA CCTACACCCT
15901 CCATGCCCCT GCTTCAGTCA CAGCAAGGTC TGGCTCAGTC TGGTGGTCCC 15951 TGACTCTGCC CACTGTCCCC ACCCTTCCAG ACTGTCTCCC TGCAGGAGCT 16001 GCAGCAGGAC TTTGAGAATG CGCCCCCAC CGACCCCAAC AACAACCAGA 16051 CCCCGGCTAA CGGCACCAGC GTGTCCTATA TCACCTTCAG CCCTGACAGC 16101 TCCTCACCTG CCCAGAGTGA GCCACCAGCC TCCGCTGAGG CCCCCGGCGA 16151 GCCCAGTGAC ATGCTGGCCA GCGTCCCACC CTTCGTCACC TTCCACACCC 16201 TCATCCTGGA CATGAGTGGA GTCAGCTTCG TGGACTTGAT GGGCATCAAG 16251 GCCCTGGCCA AGGTGAGGCC CTCGGGGACA GCAAGCACCA CCCACTCCAC 16301 CCCTCCGCT CTGCTCTCCA CATTCCCTTT CCTGGGAGCC CTCATTTCAG
16351 GAAGCTGAGG GAGGAAGCTC ACTGGGGAGA CTAACAGCTC CTAGGAATCC
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17001 TGAGAATCTA AGCTACTGAA AGAAAAGATC AGCCGGGCGT GGTGGCTCAC 17051 TCCTGTAATC CCAGCACTTT GGGAGGCCAA GGCAGGTGGA TCACAAGGTC 17101 AGGAGTTCAA GACCAGCCTG GCCAACATGG TGAAACCCCG CCTCTACTAA 17151 AAATACAAAA ATTAGCCAGG TGTGGTGACG GGCCCCTGTA GTCCCAGCTA 17201 CTCGGTAGGC TGAGGCAGAG AATTGCTTGA ACCCAGGAGG CGGAGGTTGC 17251 AGTGAGCCAA GATCGCGCCA CTGCACTCCA GCCTGGGCAA CAGAGTGAAA 17301 CTCCATCTCA AAAGAAAAA AAAGAAAATA TCTAGCCCCA CAAGAAGGGG 17351 CCATGGTGAC TTTAAGTGCC CGCCACGTTG GCAAAAGTCC ATTTCCGCTC
17401 CACTTCCCAG AGAAACCGTC AGCCAACACT CCAGGGAGAA GTGGTGTGCT
17451 TTGCTGCTAT TTTTGTCTTT GGCTGCTGGG CTCTCAGGGT TGCTTATTTG 17501 TTTGGCTTCC CCTCTGAAGT ACGTTTTGTG AATCACTTTT GAGACCCACT 17551 CAGAACATTC CTTTCCTTTT GCCTCCCTAC CCCAACAACA CTTCTAGCTG
17601 AGCTCCACCT ATGGGAAGAT CGGCGTGAAG GTCTTCTTGG TGAACATCCA
17651 TGGTAAGAGA AAGAGGACAT TTAGGGACTG AAAGACTGGC AAGGAGTGTG 17701 GGGTAGGAAC AGGTTGGTGG GGTCTGAATA GTGAGGAGGT TGGAAACGAG
17751 AGCACCCAGC TATCCCCCAC AAGCTGCTGC CTGCTCATAA AAGCTTCAGG
17801 TACAAGTCCA AAGAGACTGG TCAGATTGCA TAAACATCCT AGGGGCCTTA 17801 TACAAGTCCA AAGAGACTGG TCAGATTGCA TAAACATCCT AGGGGCCTTA 17851 GTGACAGAGT GGGGGTGAGG AGGTCATGGA GTTACAGAAG GACAGCTAGG 17901 ATTCTAATCT ACCCCATAAC TAATTTGCCA CGTATCCTTG GCCGAGTCAC 17951 TTTATCTCTC AAGGGATCAT TTTCTACCTA TGTAAAACGA GAGGGTTGAC 18001 TAGATGGATT TGGGGATCCT CTCCCAATCA GAAACTCTGT GAATCGATAT 18051 AGGCATAGAG CACACGGTAC CCTAATTCCC CAGGGAACAT ATAAATATGC 18101 AGTTTTGTAG GCATACAGCC TCCAAAGGGT GCATATACAC AGCCTCAAGG 18151 ACGTGGCCAC AGGGCAGCAG ACATTTACAT GACTAGCATG TACGCAAAGT 18201 GCAGAGATGT GGGAGCAAGT GCACACAGAC ACACAGGAGA ATGTGAAGGG 18251 GCACATACAC ACACACCCAG CTCCCTGCAC TGGGTCAGAC CCCCCTCCAGC 18301 AGGGCTGCAG TTCCCAAAGCT CCGCATGGC ACGTTCGGG AGAGAATCTG 18351 CAGTGGCAAT GACCTGCTAT GATATGTTCT GGAGTTAGAA GCAGTGGATT 18401 CTCCCCAACC TCACTGGACA CCCCCTTAGG AAACCATCTC TAGGATTAAG 18451 AGTAATCCAC ACAAACTTCC AATGCCACAC ATTGGAAGTT GCTGGAAAGG 18501 TCTGGGAAAA CAAGAGGAAG GATGGGTCCT TGGGGGATAG AACTGGCAGC 18501 TCTGGGAAAA CAAGAGGAAG GATGGGTCCT TGGGGGATAG AACTGGCAGC 18501 TCTGGGAAAA CAAGAGGAAG GATGGGTCCT TGGGGGATAG AACTGGCAGC
18551 GGCCTCTTCA AGGATGGCTT AGGCTTTTCC ACTCGAATCA CCACAAAGTA
18601 CTGACTCCCT AAATCAAACT GCTTCCTTCT GCTCTGGGTT GAAACTTCAG
18651 CATCCTCAAG TTCATGTTGC CCTCTGCCGT CCAGAACTGA TATTGCACTG
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18751 CCATCCCTGC TCTGGTCTCA CTATCTTCCC CACCCCCAGC TCCAATCCAC
18801 AATGGCTGTT ATCTTTCTGA AGGTGATCTT TTCTCCTTCT AGCCCAGGTG
18851 TACAATGGCA TTTCCCAGCA TACATGACGC AGTCCTCTTT GCCCAGGCAA 18901 CAAGCACGTC TTTCCCAGCA TACATGACGC AGTCCTCTTT GCCCAGGCAA
18951 ATGCTAGAGA CGTGACCCCA GGACACAACT TCCAAGGGGT AAGGTTCTTG
19001 CACCTGGGGA ATCCTAGGCT CCAAGGCACT GAAATAGCAG GACCAAGAGG 19051 CATTATTAGA AAGAACACAG GAGAAGGTTT AAGTTCCAAT ATCAAGTCTG
19101 CCATTTCAGT TTTCTGAATC TGTTTCCTTA TCTATAGAAT GAGCACCATC
19151 AACTAACAATT ACCTACCTCT CTGCATTTTT CTTTTATTTT GTTTTAGGGT 19401 CATTITAACT TACCGGAGCT TAGAGATTTC AGGCTGGTGA GGGATAAAGA 19451 GATTGGGTCT GAGTTTTGTC TCAGCTTTTT GACATTTAAT TTACTAGCTC 19501 AGTAAGTCAT ACAAATGGGA TACAAATAAC ACCATCTAAA ACTCCAGAAG 19901 CCGCAGAGCA AAGAGGGAGA TTCTGGAGGA AGCTGCATTA GTTGTTAGTG
19951 CCCTAATCAT GTTCAGCTAC TCTAGTTGGT ATGTATACTT GATTAGTCAT
20001 AGCACTTATA AATAATTTAT ATTTTATATA ATATATACTT ACATATTATA
20051 GACCATTCAC AGATACAAAT CACACACATA AACACACACC TTTTCAACAG
20101 CATTGTGAGG GACAAAGCAG GCAAAGTGAG GCTGGTTATC AGACTTTAAC
20151 AGATTAGAAA ATAATTCCC AGGAGGACAG GAATTCCCCA AGGTCAGGCA 20201 GCTAGCCAAT AGTTTTTCTA AGCTGAGTAA AACCTTCCCT GCCTCTAACG 20251 GCCCACAAAG GAGGGAAGAC CGCGATACAC ACCTGTCTGG TATAAGGGGG 20301 AAGACCACAG CCGTGCTGTT TTTGTGAGGC AGGTAAGGGA AGGGGCAAGA 20351 GGATAAGTCA TGTGTCAGGA AGCAGCGTCC AACCAGAGCC GGCCACCTGT

Docket in Serial N. Inventors: K. Title: ISOLATED H. 20401 CCCTTTCCT GCCACCATGC ACCAACTTTC 20451 ATTCTGCACT GGCTTCCTCC CTTCCAGGCT 20501 CTTGTACGAC TCAGAGGAGG ACATTCGCAC 20551 TGAGCTGAGG GAAGGGGCTG TGAGGGTGGG

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Serial No.: 09/749,589
Inventors: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER...

20401 CCCTTTTCCT GCCACCATGC ACCAACTTTG CTGTTCAGTC ACTGAAGCTC 20451 ATTCTGCACT GGCTTCCTCC CTTCCAGGCT CCAGGGGATG CTGAGCTCTC 20501 CTTGTACGAC TCAGAGGAGG ACATTCGCAG CTACTGGGAC TTAGAGCAGG 20301 CTTGTACGAC TCAGAGGAGG ACATTCGCAG CTACTGGGAC TTAGAGCAGG
20551 TGAGCTGAGG GAAGGGGCTG TGAGGGTGGG AGCAGGGCGA AGAGGGGAAG
20601 GATGGGGTCG CTGTCAAATA CAAGGCGTTC ACTCAGCTGT CTCACCTCCA
20651 GCCCAGAGCA GTCACATTCA AGGCCACAAA GATTTGTGGT CATCTTTGTT 20701 TTTTTCTTT TCCTTTTCTT TTTTTTTT TTTTAATTTG AGACAAAGTC 20751 TCACTCTATC ACCAGACTG GAATGCAGTG GCATGATCTC AGCTCACTGC
20801 AACCTCTGCC TCCCGGGTTC CAGAGGTTCT CCTGCCTCAG CCTCCCGAGT
20851 AGCTGGGACT TCAGGCCTGC GCCCAGCTAA TTTTTGTATT TTTAGTAGAG
20901 ACAGCTTTTC ACCATGTTGG CTGGGCTGGT CTCGAACTTC CGATCTCAAG
20951 CAATCTGCCT GCCTCGGTCT CCTAAGTGCC TGGATTACAG GCATAAGCCA
21001 CGATGCCTGG CCTTTGTTTT CATTCTTCT ACTCCCTGAA AGGCATCGTG 21051 GGGAGAGGGT GAGTCACTGG ACCAAGTCCT AGAGAACCAG TATCTATTCT 21101 TATTCTCCAA CACATCACCC ACGTGACCCT GAGCAAGCCA CATACACCCT 21151 GGGCCCTAGT TTTTATCATC TGTGAAATTA GGGGAAACAT AGGTAATACC 21201 TGTCCCATCC ACCACACAG ATTGGCAGGG CAGTCACTTG TTCTTTCATT 21251 AATTCAGCAG GTATTTATGG CGTACCTACT GTTTGCCTGA CACAGTTCAG 21401 NNNNNNNNN NNNNNNNNN NNNNNNGTCT ACAAATGAAT TATTATTGCA 21451 TGTGGACAGG CCTTAAGAAC TAAAAAATAT GCGAGTGGGT GCAATGGTTC
21501 ACACCTGTAA TCCCAGCACT TTGGGAGGCT GAGGTGGGCG GACCACCTGA
21551 GGTCAGGAGT TTGAGACCAG CCTGGCCAAC ATGGCGAAAC CCCGTCTCTA
21601 CTAAAAGCAC AAAAATTAGC CAGGCGTAGT GGTGCATGCC TGTAGTCCCA
21651 GCTACTCGGA AGTCTGAGGC ATGAGAATCA CTTGAACCTG GGAGGCAGAT
21701 GTTGCAGTGA GCCGAGATCG TGCCACTGCA CTCCAGCTTG GGTGACAGAG 21751 CTAGACTGTC TCAAAAACAA ACAAACAAAA CAAAACCTAA AAGATATGTG 21801 GATATGAGGG ATCACCATCC CCATAGGGCC CCTGGATTAA CACCACCCA 21851 CCAATGCCCT GAATTAAAAG AAACCAGATG ACTAGGTTTG GAGAAATCTG 21901 GCTTTGGGTC TATGAGAAGT AGTGTCTCTC TTTGTGCCTC TTCCCATTCT 21901 GCTTTGGGTC TATGAGAAGT AGTGTCTCTC TTTGTGCCTC TTCCCATTCT
21951 TTTTGACATT GAGCTCCATG GTGCTCTGAA TCCGTCTCTC ACAGTGCTGA
22001 TGGCAGGTGG GACAGATTAG AAAATAGAGC TGGAGCCACA GAGATTTGGC
22051 AGACTGATTT CGGTGCCCTC TTGGAATCTC CAGCACATTC CAAAAAGCCT
22101 GGATAGGACC AAAATAGCTT ATCAACGTGA GAAAGGACTT CAGAGCTTGT
22151 CTACTGCCAA CCCTCATTTT ACCCAATGAG GAAAGGACTT CATTAGGGG
22201 GCGAGGGACA CGTGGAAGGT CACACAGCAC ACAGGAGGTG ATTCACATGT
22251 AGATTTCAGC ACCTGCTCT GCCACGCTGG ACTGGTTCAC CTCCTAGGCT
22301 GACCCTGCCT CTCCCCTGTT CACACACACT CTCGCACACA CACACACAC
22351 CACACACACA CACAGGTGCT TTGTTCTGGC CAGGGGTTCC TAGGGTCACC
22401 TCTTGGTTGC AGCCACTGTG ACCCCAACTG GTCTAACCTC TCCTCTTCCCC 22401 TCTTGGTTGC AGCCACTGTG ACCCCAACTG GTCTAACCTC TCTCTTCCCC 22401 TCTTGGTTGC AGCCACTGTG ACCCCAACTG GTCTAACCTC TCTCTTCCCC
22401 TCCCCACTTCC TTCCTGTGGT TCCTGCAGGA GATGTTCGGG AGCATGTTTC
22501 ACGCAGAGAC CCTGACCGCC CTGTGAGGGC TCAGCCAGTC CTCATGCTGC
22551 CTACAGAGTG CCTGGCACTT GGGACTTCCA TAAAGGATGA GCCTGGGGTC
22601 ACAGGGGGTG TCGGGCGGAG GAAAGTGCAT CCCCCAGAGC TTGGGTTCCT
22651 CTCTCCTCTC CCCCTCTCTC CTCCCTTCCT TCCCTCCCCG CATCTCCAGA
22701 GAGAGCCTCT CAGCAGCAGG GGGGTGCTAC CCTTACAGGA GTGAGAGTCT 22751 GGTGAGCCCA CTCTTCACCC GTCAGGCCCT GGCCGCAATG GACAAGCCTC
22801 CTGCTCACTC CACCCCACCC ACCTCTGCCC TGTCCTTGGC AGCTGAAGGA
22851 CACCTGACT TCCAGCTTTT ACGAGTGAGC CAAAAACAGA AGGACAAGTA 22901 CAACTGTGCT GGCCTGCTGT ACAAGCTTCA AAAAGTGTCC CAGAGCCCAC 22951 ACGGCTCGGT GTCAGATGGT GTCAGGCTTCA AAAAGTGTCC CAGAGCCCAC
22951 ACGGCTCGGT GTCAGATGGT GTCAGGCTGT CACGGACATA GGGATAAACT
23001 TGGTTAGGAC TCTGGCTTGC CTTCCCCAGC TGCCTCAACT CTGTCTCTGG
23051 CAGCTCTGCA CCCAGGGACC ATGTGCTCTC CACACCCAGG AGTCTAGGCC
23101 TTGGTAACTA TGCGCCCCCC GTCCATCATC CCCAAGGCTG CCCAAACCAC
23151 CACTGCTGTC AGCAAGCACA TCAGACTCTA GCCTAGACCAC TAAGGTTCTG
23201 CGTCGAGACC ACCAGAACCAC ACTGCCCTCA GAGGCTGCTC CCTTCCCCTG
23301 GAGGCTGGCT AGAAACCCCA AAGAGGGGGA TGGGTAGCTG GCAGAATCAT 23301 GAGGCTGGCT AGAAACCCCA AAGAGGGGGA TGGGTAGCTG GCAGAATCAT 23351 CTGGCATCCT AGTAATAGAT ACCAGTTATT CTGCACAAAA CTTTTGGGAA 23401 TTCCTCTTG CACCCAGAGA CTCAGAGGGG AAGAGGGTGC TAGTACCAAC 23451 ACAGGAAAA CGGATGGAC CTGGGCCCAG ACAGTCCCCC TTGACCCCAG
23501 GGCCCATCAG GGAAATGCCT CCCTTTGGTA AATCTGCCTT ATCCTTCTT
23551 ACCTGGCAAA GAGCCAATCA TGTTAACTCT TCCTTATCAG CCTGTGGCCC 23601 AGAGACACAA TGGGGTCCTT CTGTAGGCAA AGGTGGAAGT CCTCCAGGGA 23651 TCCGCTACAT CCCCTAACTG CATGCAGATG TGGAAAGGGG CTGATCCAGA 23701 TTGGGTCTTC CTGCACAGGA AGACTCTTTA ACACCCTTAG GACCTCAGGC 23751 CATCTTCTCC TATGAAGATG AAAATAGGGG TTAAGTTTTC CATATGTACA



23801 AGGAGGTATT GAGAGGAACC CTACTGTTGA CTTGAAAATA AATAGGTTCC 23851 ATGTGTAAGT GTTTTGTAAA ATTTCAGTGG AAATGCACAG AAAATCTTCT 23901 GGCCTCTCAT CACTGCTTTT CTCAAGCTTC TTCAGCTTAA CAACCCCTTC 23951 CCTAACAGGT TGGGCTGGCC CAGCCTAGGA AAACATCCCC ATTTCTAACT 24001 TCAGCCAGAC CTGCGTTGTG TGTCTGTGTG TTGAGTGAGC TGGTCAGCTA 24051 ACAAGTCTTC TTAGAGTTAA AGGAGGGGGT GCTGGCCAAG AGCCAACACA 24101 TTCTTGGCCC AGGAGCATTG CTTTTCTGTG AATTCATTAT GCCATCTGGC 24151 TGCCAATGGA ACTCAAAACT TGGAAGGCGA AGGACAATGT TATCTGGGAT 24201 TCACCGTGCA CAGCACCCGA AGTGCCAAAT TCCAGGAGGA CAAGAGCCTT 24251 AGCCAATGAC AACTCACTCT CCCCTACTCC ACCTCCTTCC AAGTCCAGCT 24301 CAGGCCCAGG AGGTGGGAGA AGGTCACAGA GCCTCAGGAA TTTCCAAGTC 24351 AGAGTCCCCT TTGAACCAAG TATCTAGATC CCCTGAGGAC TTGATGAAGT 24401 GATCCTTAAC CCCCAAGTAA TCATTAACCC CCAGACCAGC CTCAGAACTG 24451 AAGGAGATTG TTGACCCAGT GACCTGGAGT TGAGGCTCAG GGAGAGATCT 24501 GCCACATGTC TGAGGGTTGC AGAGCC (SEQ ID NO:3)

FEATURES:

1997 Start: 1997-2121 Exon: 2122-4732 Intron: 4733-4872 Exon: 4873-5004 Intron: 5005-5115 Exon: 5116-5781 Intron: 5782-5957 Exon: 5958-7770 Intron: 7771-7935 Exon: Intron: 7936-8470 8471-8623 Exon: 8624-8917 Intron: Exon: 8918-9000 9001-9777 Intron: Exon: 9778-9925 9926-10221 Intron: 10222-10335 Exon: 10336-10539 Intron: 10540-10617 Exon: Intron: 10618-11197 11198-11293 Exon: 11294-13338 Intron: 13339-13445 Exon: 13446-14214 Intron: 14215-14284 Exon: 14285-14400 Intron: Exon: 14401-14493 14494-15980 Intron: 15981-16262 Exon: Intron: 16263-17597 17598-17652 Exon: 17653-18842 Intron: 18843-18988 Exon: 18989-20477 Intron: 20478-20549 Exon: 20550-22478 Intron: 22479-22523 Exon:

CHROMOSOME MAP POSITION:

22524

Chromosome 1

Stop:

ALLELTC VARTANTS (CNDC)

DNA Protein	
Position Major Minor Domain Position Major	Minor
48 C G Beyond ORF(5')	
132 G A Beyond ORF(5')	
724 A C Beyond ORF(5')	
1558 C G Beyond ORF(5')	

FIGURE 3H



1577	Α	G	Beyond	ORF(5')			
2487	C	Α	Intron				
2634	Т	C	Intron				
4352	Α	G	Intron				
5157	Α	C	Intron				
5658	Α	Ť	Intron				
5945	Т	c	Exon		180	Т	т
6281	Ċ	C T	Intron				
6452	Ğ	Ċ	Intron				
6610	Ť	Ğ	Intron				
7247	Ť	č	Intron				
7360	À	C G	Intron				
7644	Ä	Ť	Intron				
8127	Â	ċ	Intron				
8317	Ĝ	Ä	Intron				
9079	Ğ	Ä	Intron				
9537	Ğ	Ť	Intron				
12302	č	Ġ	Intron				
12354	č	T	Intron				
12487	č	τ̈́	Intron				
13198	-	Ä	Intron				
13257		Ĝ	Intron				
14541	A G	A	Intron				
14545		G	Intron				
15041	A C		Intron				
		A	Intron				
15053	A	C					
15065	A	G	Intron				
15108	Α	C	Intron				
16274	-	G	Intron				
17424	c	Ţ	Intron		CEZ		.,
17627	G	A	Exon		657	V	V
18427	Ţ	C G	Intron				
18813	C	G	Intron				
19035	Т	C C G C	Intron		•		
19182	Т	Ç	Intron				
19508	-	GC	Intron				
19571	Т	GC	Intron				
20147	T	G	Intron				
20180	· G	Α	Intron				
20584	Α	Т	Intron				
20717	T	С	Intron				
20894	Α	G	Intron				
21787	-	A C	Intron				
22264	T	С	Intron				
22338	-	CA	Intron				
23363	Т	С		ORF(3')			
23688	G	A C		ORF(3')			
24210	Α	C	Beyond	ORF(3')			
			-				

Context:

DNA Position

CTGGGTTCCTATGTGGGGAGGTCATGCTCCCCACTCATTGAGCCCCC

[C,G]

CAGGCAAACCACCTGGACAGCCAGACCCATGCAGACTCTGGAGCAGGTGGAGAGAAGAG TGAGACCACCCCGCCTCACGGGCGGTGAAGGGCCGGCAGCCTCTGAATAGTCTCTGCTAG GAGGTAGAAAGCACCCTCCCATCTTAATCATAGTAATCATCGCCACTACCATTTACTGGG TGCCTATAAAAGGCCAGCCTCTTCATACACATGATCTCACTGAATCCTCATAGCATCTGC CTGCGACTGTTATTATCCCCATTTACAGATGAAGAAACTGAATCTTTGAACCCAGGTCAT

132 CTGGGTTCCTATGTGGGGAGGTCATGCTCCCCACTCATTGAGCCCCCCCAGGCAAACCAC CTGGACAGCCAGACCCATGCAGACTCTGGAGCAGGTGGAGAGGAAGAGTGAGACCACCCC GCCTCACGGGC

[G,A]



ACAGATGAAGAAACTGAATCTTTGAACCCAGGTCATCTGGCTCTCAAACTTGTGCTGTTTTCCCTAAGCCACCCGGTCTCTCATTTCTCCCACTGAAATGTCTCACATGCCATTGCCCTT

TCACACTTTACATTTACACAACCCCTTCTTATCCATTAACTCATTIGATCTTCACAACA
ACCCTGTGAGATATGTCTTTACTCCCACTTTAGTGATACAGAATCTGAGGTTTGAAAAG
TAATGCTGACCATTCTGCCTCATTAATAAAAGCAGGATTAACCCAGGCTCCTGGACCCTT
CCACAAAAGGCATTAAGCAACCTGCTCCCCTCTGACAACCTCCCCTGTCACCCAGGCTCT
CCTCTGGGAAGTTGGGGGCATCTCTAGCCCCCAAGTAGTTACTCATTTTCAACCCCATCT

TCAGCTCTGCCCATCTCAGCTCCTGGAACGTCAGCCAGGTTGCGCAAAAAGTGAGGAGGA
GAGGAGCGGCAGTACACAAGGGTGGGGGAAAGATTAGGCACAGGAAGCCGTGGGAGAGAG
AGCCGGCAGGTGGACCATCCTGGTTTCCCCACACACACCATTGTCCCCCTGGGAAACCTG
TTGGTGAAGTTCTAGATGTCTTATCCAAGAAGGGTCCTCTTGAGGTCATCTCAGCTATCC
CCCTGCCTCTAGGCAAGCTGTTTTCTGTTTCTCAAGCTGACTGGCTGAATGGTAGGAG
[C,G]

2487 ACACGGCTTCTGCACTGGTATCCCTAAGATGGGGTTAAGGGAAGCCCTGGGGAAGTGAGG
TTCTGAATGATGATTTAAGATCCTACAACCTCATCTGTACTGAGACCCCCAGGGAGGAT
GGGGAGCAGGAGCAAGAACCATCCAGAAGGGTTATATGGCATTCCCAAACCCCTGCATGG
CATCTCCCATATTCTCAATTCACCCGGGTCTCTCTGGGTTTGTTAAGGCATGGTAGATGA
GCATCTACGTTATGGAGGGGTGGGGAGCATCAGAGCCCTTACTCCATGCCCTGTTCCCTC
[C,A]

> ACCAGCGCCCAGGGTCTTTCCACTCTCATCTCCCTGGAAATGCGATGGTGGGTATGAAAC CTTGTCCCTAAGTAGGCGCTACACAAGGTGATCCATACCCACACCCCAGGAGGCTGGGGC TGCGGGTGTCACCCTCCCCATTCCCAGACTCCTGGCAGACCTCCTCTGGCCCAGCTATAG GCCAACTCACTCTCCCTCACTCCCTTGGGGAAACGGCTGATTCAGTTACCTGGATTGAGG TCACTGGCAATGGCTGAAGTGGAGACGCAGGTGGAACTGGTTCAGGCCGGGGGAATCACC

FIGURE 3J



CAÁGGATGGGAGGTGTGGCAAAGGGGCCTCGGGAGATTTTCCATCTGCATTCTCCTGGAG
TTGTTCCTGGTCAGTCCTAGGGGAATGGTCACTGTGAATGTCATTTCCAGGTCCTCGGTG
ACCTTGGAGAAACCACTGAGCCTCTTTGAGTTCAGTTAGCATTACCTGTTCCATCTTCCT
CCTAGGAATGAGAGGAAGACTTAGCAGAACAAGATATACCATATGCTATAACATGCTTAA
ACAGATGTGAGAAATCACCATCTAACTCCCTGGTTGGTCCCAGCCGGCCACTACAGGGAC

TAGGTTTTATGAAGGGAAGCACAACATGACAGAATGCAAGAGCAAAACACAGTCCCAGAG



GGGCTCACCTCCTCCTCCCCATCCCAGGGCTAAAGTGAACCTTGAAAATTAACAGT ATCTCCTCATCTGCATGTAGCAGGACCATACAAAAAAACAACAGCTGTACCTGGTTAAAC TGTCCTGAGCTTTAAACCTGTAAAAGACTCACAGCCTCTCTCCATTATCCCGTGGAGAAA CCCAACTCTCTGCCAGCATAGTCTTGCAGACTGCTAATTTTCTCTAACATCCCTCACTCC [T,G]

7247 GACACAGAGCAGAGTCACGGAGGACCTCAAAGAGGAGGTGACACTCCACCTCTCTTAAAG
GATGAGAACTTAACCAGGAACAAGGTATACAGAGGATGGTCCAGGCAGAAGGGAACAGTG
CCTAAAAACACTGAGGCCTGAGAGAGTGTGATCTGCGCAGGCAAAGTAAGGGGCTTGGTG
TGGCTGGAGGGTAGAGGGCCCAGAAGAGGATGGAAAAGTAGGCAGGAGCCAGACAATGAG
ATCTGGGGTCTGTTCTCTGACAGCGACTTTGGGTCTGATTGGCAGTTTATAAGGATCGTT
[T,C]

GGGCTACACAATGATGAGTGGGAGGTGGATTAGAATCAAGGCAGGGGACCTGTTGGGAGA CTCTGCAGAGGCCCAGGCAGGAATAATGCAGGCGAAGACCAGGTAGAGAAAGAGATGGGG CTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGTGATAGACTGGATGTGGGAGGTAAG GGAGGATGACTCTCAAGTTTTTGGTTGGCCAACCAGGTTAATGATGGTGTCATTTACTGA GAGAGAAAACACTGGGGGAGGACTAGACTTATTTTACAGATAAGCCAAAGCCAGAGAGGT

7360 AACAGTGCCTAAAAACACTGAGGCCTGAGAGAGTGTGATCTGCGCAGGCAAAGTAAGGGG
CTTGGTGTGGCTGGAGGGTAGAGGGCCCAGAAGAGGATGGAAAAGTAGGCAGAGCCAGA
CAATGAGATCTGGGGTCTGTTCTCTGACAGCGACTTTGGGTCTGATTGGCAGTTTATAAG
GATCGTTTGGGCTACACAATGATGAGTGGGAGGTGGATTAGAATCAAGGCAGGGACCTG
TTGGGAGACTCTGCAGAGGCCCAGGCAGGAATAATGCAGGCGAAGACCAGGTAGAGAAAG
[A,G]

GATGGGGCTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGTGATAGACTGGATGTGGG AGGTAAGGGAGGATGACTCTCAAGTTTTTGGTTGGCAACCAGGTTAATGATGGTGTCAT TTACTGAGAGAGAAAACACTGGGGGAGGACTAGACTTATTTTACAGATAAGCCAAAGCCA GAGAGGTGATGTGACAGAAAGGCCCATGCTCTAAAGGAGCTGAAGGTCTGATGGCAGCCA TGTAGAGCACAGTGAAGGGCAGGTGAAGGTCACAGATGGTCCAATTCCCTCAAGCTACTG

TTCCTCAAGCTACTGCTACGCTAGGACTGCACGAGCTCCAGACCTGCGTGTGTGGGGGCGGGGTCGTTGGAACCTGCAGACCACCACTTTTCCTCCTCCTCCAGATGGGTCTGGGCTTCATGCAGTTTGGCTTTTGTGGCCATCTACCTCTCCGAGTCCTTCATCCGGGGCTTCATGACGGCCGCCGGCCTGCAGATCCTGATTTCGGTGCTCAAGTACATCTTCGGACTGACCATCCCCTCCTACACAGGCCCAGGGTCCATCGTCTTTGTGAGTCTG

FIGURE 3L



CCCCACACCAACATCGCCTCGCTCATCTTCGCTCTCATCAGCGGTGCCTTCCTGGTGCTG GTGAAGGAGCTCAATGCTCGCTACATGCACAAGATTCGCTTCCCCATCCCTACAGAGATG

9079

TTCTACTGCTCTAATAATTCCCCCTAAGGAGGCAGGGGAGTGGGATTCAGGGTCCCCAGA GAAAAGGGAGACTTGAGAGAGACGCCTGCCCTGGCCCCACCTTAGGGCCAATCCCCATTC TCCACTCTGGGGTTTGCAGGTGGTGGTGGCAACAGCTATCTCCGGGGGCTGTAAGATGCC CAAAAAGTATCACATGCAGATCGTGGGAGAAATCCAACGCGGGTGAGTCCAGGTGGCCCA GAAGCCTGGCCCACCCGCACCTCATGCCCCACTAAGGCCTGAGCTCGGAGAGGGAGACAA [G,A]

ĀTĠAĀCTCTATGAAAGTGCAGTCGAAACTGTATGACACTGACCATGTATGAATTATTACT ATTACCGTTTCCTGAGAAGGGCCGCACAACCAGCCAATGTAGGCTATTTTATGAGAAATG AGTCTTAACTGCCACACTCCCCTTATAAATCTCATTCAACTGATGCTGTTAAACAAAGCC TCTCTGAACAGCCGCTTGCTGGCTCTTTGCCTTGCTCTAATGCATTGGTTCTTTGTCCAT GTAGAAAGGGAACTATTAGGTTCAACCAGATTCATGAAGCATCCACTCTGTGCCAGGCAC

9537

AACTGATGCTGTTAAACAAAGCCTCTCTGAACAGCCGCTTGCTGGCTCTTTTGCCTTGCTC
TAATGCATTGGTTCTTTGTCCATGTAGAAAGGGAACTATTAGGTTCAACCAGATTCATGA
AGCATCCACTCTGTGCCAGGCACCATGCTGGGCCCCTGGGAGGAGAGGGGTGACGCTTGTC
CTGCAGGGTTGGAACAGGCAAGGGAGGGAAGACCACATAGCACCAAAAGGTCTAGGGGTCT
GTGGACTCGTGAGCATACAGGGTTCAGAATCTGGGAGTTAACAAACGAGGCCCTACCACA
[G,T]

12302

12354

GAAACCAAGGCTCAGAATGGTTAAGTAAATTGTCAAAGGCCACAGAGGTAGGGAGTGGTA GAGTCTGGATTAAAACTCCAAGTCCTGGACTCCAGACCTCTAGGCTGTACTGTCTCATAG GGAAGGCAGTCTCACCCACCTAGGGCAGAGAAGAAAATCCTTAAAGCCAGAGAAGTGAGT GGCTCATCTGTGGTCACCCAGAGAGACAGTGATGAGGACAGGGAGAAAAATTATACCTCA GTTCCCAGCCCAAGGATCTGCTTTGACCATAACCCAACAAGCCCCCGCTATGGTGGTATT

12487

13198

FIGURE 3M



[-,A]
AAAATGCTATTTAAAGAAAAAAAAGAGAAGAGAGGCTCTGAGGTTGTACTAACAGAGAAT
GGCCTTGGCTAATCCAGGAAGACTTCCTGAAAGAGGTTGTTTTTTCCCCAGGTCTGCTTT
TGACATCTCTCTTTTCACAGTGCATCTGGGTAGTGAGCTTCCTCCTCCTTCTTCCTCA
GCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGTCCTGGTCGTCGTCGTCAGA
CTCAGTTGTAAGTGATAGCTTCCGCCCTCCTAGGCCCACAGTCGGTTCCCTGGGCCAGCC

TGGCCTTGGCTAATCCAGGAAGACTTCCTGAAAGAGGTTGTTTTTTCCCCAGGTCTGCTT
TTGACATCTCTCTTTTCACAGTGCATCTGGGTAGTGAGCTTCCTCCTCCTCCTCCTCCTC
AGCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGGTCGTCGTGGTCTTCCAG
ACTCAGTTGTAAGTGATAGCTTCCGCCCTCCTAGGCCCACAGTCGGTTCCCTGGGCCAGC
CCGCAAAGGGCTTCCATGCCACGGCCTGGCTTAGTCCACCTTCCACCTCTGGGCC

CTCCTGCCCATTCTGATACTGCCCCCTGTTACTCATGGTACCCTGGGGGCCCCGCTTCCC

> CTTGGATGAGGTGCTACCATCTCCCAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCAT TTTCTGGCTAAGATAGGACATGGCCCATGGACTTTTGAACAACCCAGAGGGGGAACAGCA

15065 CAGCCCCGTGCCCTGCTCTCCTGCCCATTCTGATACTGCCCCCTGTTACTCATGGTACCC



CCCAGCTAATTTTTGTATTTTTAGTAGATATTGGGTTTCACCATGTTGGCCAGGCTGGTG
TCAAACTCCTGACCTCAGGTGATCCACCTACCTTAGCCTTCCAAAGTGCTGGGATTACAA
GCCTGAGCCACTGCGCCCAGCCTGGGCATTTTTCTTCTTGGATGAGGTGCTACCATCTCC
CAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCATTTTCTGGCTAAGATAGGACATGGC
CCATGGACTTTTGAACAACCCAGAGGGGGAACAGCAGTGAATTTCCTGGGGAACCCAGGC

- GGGTGCATATACACAGCCTCAAGGACGTGGCCACAGGGCAGCAGACATTTACATGACTAG
 CATGTACGCAAAGTGCAGAGATGTGGGAGCAAGTGCACACAGACACACAGAGAATGTGA
 AGGGGCACATACACACACCCCAGCTCCCTGCACTGGGTCAGACCCCCTCCAGCAGGGCT
 GCAGTTCCCAAGCTCCGCATGGCCACGTTCGGGGAGAGAATCTGCAGTGGCAATGACCTG
 CTATGATATGTTCTGGAGTTAGAAGCAGTGGATTCTCCCCAACCTCACTGGACACCCCCT
 [T, C]
 AGGAAACCATCTCTAGGATTAAGAGTAATCCACACAAACTTCCAATGCCACACATTGGAA
 GTTGCTGGAAAGGTCTGGGAAAACAAGAGGAAGGATGGTCCTTGGGGGATAGAACTGGC

FIGURE 30

AGCGGCCTCTTCAAGGATGGCTTAGGCTTTTCCACTCGAATCACCACAAAGTACTGACTC



CCTAAATCAAACTGCTTCCTTCTGCTCTGGGTTGAAACTTCAGCATCCTCAAGTTCATGT TGCCCTCTGCCGTCCAGAACTGATATTGCACTGCCAATGCCATGCCCTCAGATACAGCA

TTTCTGAAGGTGATCTTTTCTCCTTCTAGCCCAGGTGTACAATGACATTAGCCATGGAGG CGTCTTTGAGGATGGGAGTCTAGAATGCAAGCACGTCTTTCCCAGCATACATGACGCAGT CCTCTTTGCCCAGGCAAATGCTAGAGACGTGACCCCAGGACACAACTTCCAAGGGGTAAG GTTCTTGCACCTGGGGAATCCTAGGCTCCAAGGCACTGAAATAGCAGGACCAAGAGGCAT TATTAGAAAGAACACAGGAGAGAGGTTTAAGTTCCAATATCAAGTCTGCCATTTCAGTTTT

19035 GGACCTCAGGCCTCTCCCATCCCTGCTCTGGTCTCACTATCTTCCCCACCCCCAGCTCCA
ATCCACAATGGCTGTTATCTTTCTGAAGGTGATCTTTTCTCCTTCTAGCCCAGGTGTACA
ATGACATTAGCCATGGAGGCGTCTTTGAGGATGGAGTCTAGAATGCAAGCACGTCTTTC
CCAGCATACATGACGCAGTCCTCTTTGCCCAGGCAAATGCTAGAGACGTGACCCCAGGAC
ACAACTTCCAAGGGGTAAGGTTCTTGCACCTGGGGAATCCTAGGCTCCAAGGCACTGAAA
[T,C]

AGCAGGACCAAGAGGCATTATTAGAAAGAACACAGGAGAAGGTTTAAGTTCCAATATCAA
GTCTGCCATTTCAGTTTTCTGAATCTGTTTCCTTATCTATAGAATGAGCACCATCAACTA
ACATTACCTACCTCTCTGCATTTTTCTTTTATTTTTGTTTTAGGGTTAAATGATAATTACA
TCTTTTGTGTCACTTGAAAGCACTTTGTGTATTGTAAAAATTCTTTATCAATATAAGTTT
TCTGGTTGCACAAACACCCAAAGCATAGTAGAGCAGGCCCACTCTGCTGGCATCGTTCCC

FIGURE 3P



> GAATTCCCCAAGGTCAGGCAGCTAGCCAATAGTTTTTCTAAGCTGAGTAAAACCTTCCCT GCCTCTAACGGCCCACAAAGGAGGGAAGACCGCGATACACACCTGTCTGGTATAAGGGGG AAGACCACAGCCGTGCTGTTTTTGTGAGGCAGGTAAGGGAAGGGGCAAGAGGATAAGTCA TGTGTCAGGAAGCAGCGTCCAACCAGAGCCGGCCACCTGTCCCTTTTCCTGCCACCATGC ACCAACTTTGCTGTTCAGTCACTGAAGCTCATTCTGCACTGGCTTCCCCCTTCCAGGCT

GGTTCTCCTGCCTCAGCCTCCGAGTAGCTGGGACTTCAGGCCTGCGCCCAGCTAATTTT

GTAGAGACAGCTTTTCACCATGTTGGCTGGCTGGTCTCGAACTTCCGATCTCAAGCAAT CTGCCTGCCTCGGTCTCCTAAGTGCCTGGATTACAGGCATAAGCCACGATGCCTGGCCTT TGTTTTCATTCTTCACTCCCTGAAAGGCATCGTGGGGAGAGGGTGAGTCACTGGACCA AGTCCTAGAGAACCAGTATCTTATTCTTATTCTCCAACACATCACCCACGTGACCCTGAGC AAGCCACATACACCCTGGGCCCTAGTTTTTATCATCTGTGAAATTAGGGGAAACATAGGT

TAAAAGATATGTGGATATGAGGGATCACCATCCCCATAGGGCCCCTGGATTAACACCACC CCACCAATGCCCTGAATTAAAAGAAACCAGATGACTAGGTTTTGGAGAAATCTGGCTTTTGG GTCTATGAGAAGTAGTGTCTCTTTTTGTGCCTCTTTCCCATTCTTTTTTGACATTGAGATCCC ATGGTGCTCTGAATCCGTCTCTCACAGTGCTGATGGCAGGTGGGACAGATTAGAAAATAG AGCTGGAGCCACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTTGGAATCTCCAGCACA

22264 CTCCATGGTGCTCTGAATCCGTCTCTCACAGTGCTGATGGCAGGTGGGACAGATTAGAAA



Docket No.: CL000861 Serial No.: 09/749,589 Inventors: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER...

ATAGAGCTGGAGCCACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTGGAATCTCCAG CACATTCCAAAAAGCCTGGATAGGACCAAAATAGCTTATCAACGTGAGAAAGGACTTCAG AGCTTGTCTACTGCCAACCCTCATTTTACCCAATGAGGAAAGTGAAGCTATTAGGGGGCG AGGGACACGTGGAAGGTCACACAGCACACAGGAGGTGATTCACATGTAGATTTCAGCACC [T,C]

ĞCTCCTGCCACGCTGGACTGGTTCACCTCCTAGGCTGACCCTGCCTCTCCCCTGTTCACA CACACTCTCGCACACACACACACACACACACACACAGGTGCTTTGTTCTGGCCAGG GGTTCCTAGGGTCACCTCTTGGTTGCAGCCACTGTGACCCCAACTGGTCTAACCTCTCTC TTCCCCTCCACTTCCTTCCTGTGGTTCCTGCAGGAGATGTTCGGGAGCATGTTTCACGC AGAGACCCTGACCGCCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTG

22338 ACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTGGAATCTCCAGCACATTCCAAAAAG CCTGGATAGGACCAAAATAGCTTATCAACGTGAGAAAGGACTTCAGAGCTTGTCTACTGC CAACCCTCATTTTACCCAATGAGGAAAGTGAAGCTATTAGGGGGCGAGGGACACGTGGAA GGTCACACAGCACAGGAGGTGATTCACATGTAGATTTCAGCACCTGCTCCTGCCACGC [-,C,A]

CACACACACACACACACACACAGGTGCTTTGTTCTGGCCAGGGGTTCCTAGGGTCA CCTCTTGGTTGCAGCCACTGTGACCCCAACTGGTCTAACCTCTCTTCCCCTCCCACTT CCTTCCTGTGGTTCCTGCAGGAGATGTTCGGGAGCATGTTTCACGCAGAGACCCTGACCG CCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTGGCACTTGGGACTTC CATAAAGGATGAGCCTGGGGTCACAGGGGGGTGTCGGGCGGAGGAAAGTGCATCCCCCAGA

23363 CAGGGACCATGTGCTCTCCACACCCAGGAGTCTAGGCCTTGGTAACTATGCGCCCCCCGT CTGGACAGTGGCCAGGACCGTCGAGACCACCAGAGCTACCTCCCCGGGGACAGCCCACTA AGGTTCTGCCTCAGCCTCCTGAAACATCACTGCCCTCAGAGGCTGCTCCCTTCCCCTGGA GGCTGGCTAGAAACCCCAAAGAGGGGGATGGGTAGCTGGCAGAATCATCTGGCATCCTAG

> AATAGATACCAGTTATTCTGCACAAAACTTTTGGGAATTCCTCTTTGCACCCAGAGACTC AGAGGGGAAGAGGGTGCTAGTACCAACACAGGGAAAACGGATGGGACCTGGGCCCAGACA GTCCCCTTGACCCCAGGGCCCATCAGGGAAATGCCTCCCTTTGGTAAATCTGCCTTATC CTTCTTTACCTGGCAAAGAGCCAATCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGA GACACAATGGGGTCCTTCTGTAGGCAAAGGTGGAAGTCCTCCAGGGATCCGCTACATCCC

23688 AAACTTTTGGGAATTCCTCTTTGCACCCAGAGACTCAGAGGGGAAGAGGGTGCTAGTACC AACACAGGGAAAACGGATGGGACCTGGGCCCAGACAGTCCCCCTTGACCCCAGGGCCCAT CAGGGAAATGCCTCCCTTTGGTAAATCTGCCTTATCCTTCTTTACCTGGCAAAGAGCCAA TCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGAGACACAATGGGGTCCTTCTGTAGG [G,A]

GGCTGATCCAGATTGGGTCTTCCTGCACAGGAAGACTCTTTAACACCCTTAGGACCTCAG GCCATCTTCTCCTATGAAGATGAAAATAGGGGTTAAGTTTTCCATATGTACAAGGAGGTA TTGAGAGGAACCCTACTGTTGACTTGAAAATAAATAGGTTCCATGTGTAAGTGTTTTGTA AAATTTCAGTGGAAATGCACAGAAAATCTTCTGGCCTCTCATCACTGCTTTTCTCAAGCT TCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGCCCAGCCTAGGAAAACATCC

24210 TCACTGCTTTTCTCAAGCTTCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGC CCAGCCTAGGAAAACATCCCCATTTCTAACTTCAGCCAGACCTGCGTTGTGTGTCTGTGT GTTGAGTGAGCTGGTCAGCTAACAAGTCTTCTTAGAGTTAAAGGAGGGGGGTGCTGGCCAA GAGCCAACACTTCTTGGCCCAGGAGCATTGCTTTTCTGTGAATTCATTATGCCATCTGG CTGCCAATGGAACTCAAAACTTGGAAGGCGAAGGACAATGTTATCTGGGATTCACCGTGC [A,C]

CCCCTACTCCACCTCCTTCCAAGTCCAGCTCAGGCCCAGGAGGTGGGAGAAGGTCACAGA GCCTCAGGAATTTCCAAGTCAGAGTCCCCTTTGAACCAAGTATCTAGATCCCCTGAGGAC TTGATGAAGTGATCCTTAACCCCCAAGTAATCATTAACCCCCAGACCAGCCTCAGAACTG AAGGAGATTGTTGACCCAGTGACCTGGAGTTGAGGCTCAGGGAGAGATCTGCCACATGTC

FIGURE 3R